SEQUENCE LISTING

	(1) GEI	NERAL INFORMATION:
5	(i)	APPLICANT: Baker, Joffre Chien, Kenneth King, Kathleen Pennica, Diane Wood, William
10	(ii) Therefo	TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses
15	(iii)	NUMBER OF SEQUENCES: 8
20	(iv)	CORRESPONDENCE ADDRESS: (A) ADDRESSEE: Genentech, Inc. (B) STREET: 460 Point San Bruno Blvd (C) CITY: South San Francisco (D) STATE: California (E) COUNTRY: USA (F) ZIP: 94080
25 0 0 0 0	(v)	COMPUTER READABLE FORM: (A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: patin (Genentech)
30	(vi)	CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: (B) FILING DATE: 05-AUG-1994 (C) CLASSIFICATION:
35 35 2	(vii)	PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: 08/233609 (B) FILING DATE: 25-APR-1994
40	(viii)	ATTORNEY/AGENT INFORMATION: (A) NAME: Hasak, Janet E. (B) REGISTRATION NUMBER: 28,616 (C) REFERENCE/DOCKET NUMBER: 894P1
45	(ix)	TELECOMMUNICATION INFORMATION: (A) TELEPHONE: 415/225-1896 (B) TELEFAX: 415/952-9881 (C) TELEX: 910/371-7168
50	(2) IN	FORMATION FOR SEQ ID NO:1:
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 1352 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5 GGATAAGCCT GGGGCCAGCA TGAGCCAGAG GGAGGGAAGT CTGGAAGACC 50 ACCAGACTGA CTCCTCAATC TCATTCCTAC CCCATTTGGA GGCCAAGATC 100 10 CGCCAGACAC ACAACCTTGC CCGCCTCCTG ACCAAATATG CAGAACAACT 150 15 TCTGGAGGAA TACGTGCAGC AACAGGGAGA GCCCTTTGGG CTGCCGGGCT 200 TCTCACCACC GCGGCTGCCG CTGGCCGGCC TGAGTGGCCC GGCTCCGAGC 250 20 CATGCAGGGC TACCGGTGTC CGAGCGGCTG CGGCAGGATG CAGCCGCCCT 300 1 GAGTGTGCTG CCCGCGCTGT TGGATGCCGT CCGCCGCCGC CAGGCGGAGC 350 __25 m TGAACCCGCG CGCCCCGCGC CTGCTGCGGA GCCTGGAGGA CGCAGCCCGC 400 LF. 30 CAGGTTCGGG CCCTGGGCGC CGCGGTGGAG ACAGTGCTGG CCGCGCTGGG 450 CGCTGCAGCC CGCGGGCCCG GGCCAGAGCC CGTCACCGTC GCCACCCTCT 500 FL 1 35 1 35 TCACGGCCAA CAGCACTGCA GGCATCTTCT CAGCCAAGGT GCTGGGGTTC 550 CACGTGTGCG GCCTCTATGG CGAGTGGGTG AGCCGCACAG AGGGCGACCT 600 40 GGGCCAGCTG GTGCCAGGGG GCGTCGCCTG AGAGTGAATA CTTTTTCTTG 650 TAAGCTCGCT CTGTCTCGCC TCTTTGGCTT CAAATTTTCT GTCTCTCCAT 700 45 CTGTGTCCTG TGTGTTCTTG GGCTGTCCCT ATCTTTCTGC ATTTGTGTGG 750 50 TCTCTCTCTT CTGCTCTCT CTCTGCAGGG AGCTTCTTTT TTCCAACAGT 800 TTCTCGTTTT GTCTCTCC AGTCTTGAAC ACTTTTGTCT CCGAGAGGTC 850

	TCTTTTTGTT	TCCTTGTCTC	TTGGTTCTTT	CTTTGCTTGC	TTGCTTGCTT	900
5	GCTTGCTTGT	TGTTGAGACA	GGGTCTCACC	ATATAGCTCT	GGATGGCCTG	950
	GAACTTGCTA	TGTAGGCCAG	GCTGGCCTCC	AGCTCATAGA	GATCCACTTG	1000
10	CCTCCGACTC	CCAATTTCCC	CATCTGTCTC	CCTGTGATCC	ATATGGGTAT	1050
15	GTGTAACCCT	TACTTTGTCT	CATGGAGGTG	ACAATTTTTC	TCCCTTCAGT	1100
	TTCTTTGTTC	TTTACTGACC	AGAAAAGTGC	CTACTTGTCC	CCTGGTGGCA	1150
20	AGGCCATTCA	CCTTAGGACC	TTCCCACCAG	TTCCTTTGTA	GGCAAATCCC	1200
AND THE STATE OF T	TCCCCCTTTG	AGGTCCTTCC	CTTTCATACC	GCCCTAGGCT	GGTCAATGGA	1250
0 0 0 0 0	GAGAGAAAGG	CAGAAAAACA	TCTTTAAAGA	GTTTTATTTG	AGAATAAATT	1300
1 30	AATTTTTGTA	AATAAAATGT	TTAACAATAA	AACTAAACTT	TTATGAAAAA	1350
	AA 1352					
11 12 13 13 13	(2) INFORMA	TION FOR SE	Q ID NO:2:			

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1352 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCTATTCGGA CCCCGGTCGT ACTCGGTCTC CCTCCCTTCA GACCTTCTGG 50 50 TGGTCTGACT GAGGAGTTAG AGTAAGGATG GGGTAAACCT CCGGTTCTAG 100 GCGGTCTGTG TGTTGGAACG GGCGGAGGAC TGGTTTATAC GTCTTGTTGA 150

AGACCTCCTT ATGCACGTCG TTGTCCCTCT CGGGAAACCC GACGGCCCGA 200 AGAGTGGTGG CGCCGACGGC GACCGGCCGG ACTCACCGGG CCGAGGCTCG 250 5 GTACGTCCCG ATGGCCACAG GCTCGCCGAC GCCGTCCTAC GTCGGCGGGA 300 CTCACACGAC GGGCGCGACA ACCTACGGCA GGCGGCGGCG GTCCGCCTCG 350 10 ACTTGGGCGC GCGGGGCGCG GACGACGCCT CGGACCTCCT GCGTCGGGCG 400 15 GTCCAAGCCC GGGACCCGCG GCGCCACCTC TGTCACGACC GGCGCGACCC 450 GCGACGTCGG GCGCCCGGGC CCGGTCTCGG GCAGTGGCAG CGGTGGGAGA 500 20 AGTGCCGGTT GTCGTGACGT CCGTAGAAGA GTCGGTTCCA CGACCCCAAG 550 GTGCACACGC CGGAGATACC GCTCACCCAC TCGGCGTGTC TCCCGCTGGA 600 CCCGGTCGAC CACGGTCCCC CGCAGCGGAC TCTCACTTAT GAAAAAGAAC 650 ₫30 ATTCGAGCGA GACAGAGCGG AGAAACCGAA GTTTAAAAGA CAGAGAGGTA 700 GACACAGGAC ACACAAGAAC CCGACAGGGA TAGAAAGACG TAAACACACC 750 ₫35 AGAGAGAAA GACGAGAGA GAGACGTCCC TCGAAGAAAA AAGGTTGTCA 800 AAGAGCAAAA CAGAGAGGG TCAGAACTTG TGAAAACAGA GGCTCTCCAG 850 40 45 CGAACGAACA ACAACTCTGT CCCAGAGTGG TATATCGAGA CCTACCGGAC 950 CTTGAACGAT ACATCCGGTC CGACCGGAGG TCGAGTATCT CTAGGTGAAC 1000 50 GGAGGCTGAG GGTTAAAGGG GTAGACAGAG GGACACTAGG TATACCCATA 1050

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	CACATTGGGA ATGAAACAGA GTACCTCCAC TGTTAAAAAG AGGGAAGTCA	1100												
5	AAGAAACAAG AAATGACTGG TCTTTTCACG GATGAACAGG GGACCACCGT	1150												
	TCCGGTAAGT GGAATCCTGG AAGGGTGGTC AAGGAAACAT CCGTTTAGGG :	1200												
10	AGGGGGAAAC TCCAGGAAGG GAAAGTATGG CGGGATCCGA CCAGTTACCT	1250												
	CTCTCTTTCC GTCTTTTGT AGAAATTCT CAAAATAAAC TCTTATTTAA	1300												
15	TTAAAAACAT TTATTTTACA AATTGTTATT TTGATTTGAA AATACTTTTT	1350												
20	TT 1352													
25 T T T	(2) INFORMATION FOR SEQ ID NO:3: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 203 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear													
₩ 30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:													
	Met Ser Gln Arg Glu Gly Ser Leu Glu Asp His Gln Thr Asp 1 5 10	Ser 15												
1 1	Ser Ile Ser Phe Leu Pro His Leu Glu Ala Lys Ile Arg Gln 20 25	Thr 30												
40	His Asn Leu Ala Arg Leu Leu Thr Lys Tyr Ala Glu Gln Leu 35 40	Leu 45												
40	Glu Glu Tyr Val Gln Gln Gln Gly Glu Pro Phe Gly Leu Pro 50 55	Gly 60												
45	Phe Ser Pro Pro Arg Leu Pro Leu Ala Gly Leu Ser Gly Pro 65 70	Ala 75												
	Pro Ser His Ala Gly Leu Pro Val Ser Glu Arg Leu Arg Gln 80 85	Asp 90												
50	Ala Ala Ala Leu Ser Val Leu Pro Ala Leu Leu Asp Ala Val 95 100	Arg												
	Arg Arg Gln Ala Glu Leu Asn Pro Arg Ala Pro Arg Leu Leu 110 115	Arg 120												

	Ser	Leu	Glu	Asp	Ala 125	Ala	Arg	Gln	Val	Arg 130	Ala	Leu	Gly	Ala	Ala 135
5	Val	Glu	Thr	Val	Leu 140	Ala	Ala	Leu	Gly	Ala 145	Ala	Ala	Arg	Gly	Pro 150
	Gly	Pro	Glu	Pro	Val 155	Thr	Val	Ala	Thr	Leu 160	Phe	Thr	Ala	Asn	Ser 165
10	Thr	Ala	Gly	Ile	Phe 170	Ser	Ala	Lys	Val	Leu 175	Gly	Phe	His	Val	Cys 180
	Gly	Leu	Tyr	Gly	Glu 185	Trp	Val	Ser	Arg	Thr 190	Glu	Gly	Asp	Leu	Gly 195
15	Gln	Leu	Val	Pro	Gly 200	Gly	Val	Ala 203							
20	(2) I	NFOE	RMAT	ION I	FOR S	SEQ :	ID N	0:4:							
5 5 6 7 7 7 7 8	(i	() ()	A) L1 3) T	NCE (ENGTI YPE: OPOL(H: 20 ami	00 at	mino cid		ds						
active ac	(x)	L) SI	EQUE!	NCE 1	DESC	RIPT	ION:	SEQ	ID	NO:4	:				
	Met 1	Ala	Phe	Thr	Glu 5	His	Ser	Pro	Leu	Thr 10	Pro	His	Arg	Arg	Asp 15
-	Leu	Cys	Ser	Arg	Ser 20	Ile	Trp	Leu	Ala	Arg 25	Lys	Ile	Arg	Ser	Asp 30
35 -	Leu	Thr	Ala	Leu	Thr 35	Glu	Ser	Tyr	Val	Lys 40	His	Gln	Gly	Leu	Asn 45
The state of the s	Lys	Asn	Ile	Asn	Leu 50		Ser	Ala	Asp	Gly 55	Met	Pro	Val	Ala	Ser 60
40	Thr	Asp	Gln	Trp	Ser 65		. Leu	Thr	Glu	Ala 70		Arg	Leu	Gln	Glu 75
	Asn	Leu	Gln	Ala	Tyr 80		Thr	Phe	His	Val 85		Leu	Ala	Arg	Leu 90
45	Leu	Glu	Asp	Gln	Gln 95		His	s Phe	e Thr	Pro 100	Thr	Glu	Gly	Asp	Phe 105
50	His	Gln	Ala	ılle	His		Lev	ı Lev	ı Lev	Gln 115		Ala	Ala	Phe	Ala 120
	Tyr	Gln	ıle	e Glu	Glu 125		ı Met	: Ile	e Leu	Leu 130	ı Glu	Tyr	Lys	Ile	Pro

	Arg Asn Glu Ala Asp Gly Met Pro Ile Asn Val Gly Asp Gly Gly 140 145 150
5	Leu Phe Glu Lys Lys Leu Trp Gly Leu Lys Val Leu Gln Glu Leu 155 160 165
	Ser Gln Trp Thr Val Arg Ser Ile His Asp Leu Arg Phe Ile Ser 170 175 180
10	Ser His Gln Thr Gly Ile Pro Ala Arg Gly Ser His Tyr Ile Ala 185 190 195
15	Asn Asn Lys Lys Met 200
13	(2) INFORMATION FOR SEQ ID NO:5:
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 50 bases(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
	GCGGCCGCGA GCTCGAATTC TTTTTTTTT TTTTTTTTT TTTTTTTTT 50
3 0	(2) INFORMATION FOR SEQ ID NO:6:
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1018 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
	GTGAAGGGAG CCGGGATCAG CCAGGGGCCA GCATGAGCCG GAGGGAGGGA 50
45	AGTCTGGAAG ACCCCCAGAC TGATTCCTCA GTCTCACTTC TTCCCCACTT 100
	GGAGGCCAAG ATCCGTCAGA CACACAGCCT TGCGCACCTC CTCACCAAAT 150
50	ACGCTGAGCA GCTGCTCCAG GAATATGTGC AGCTCCAGGG AGACCCCTTC 200
	GGGCTGCCCA GCTTCTCGCC GCCGCGGCTG CCGGTGGCCG GCCTGAGCGC 250

		CCCGGCTCCG	AGCCACGCGG	GGCTGCCAGT	GCACGAGCGG	CTGCGGCTGG	300
	5	ACGCGGCGGC	GCTGGCCGCG	CTGCCCCCGC	TGCTGGACGC	AGTGTGTCGC	350
		CGCCAGGCCG	AGCTGAACCC	GCGCGCGCCG	CGCCTGCTGC	GCCGCCTGGA	400
	10	GGACGCGGCG	CGCCAGGCCC	GGGCCCTGGG	CGCCGCCGTG	GAGGCCTTGC	450
	15	TGGCCGCGCT	GGGCGCCGCC	AACCGCGGGC	CCCGGGCCGA	GCCCCCGCC	500
		GCCACCGCCT	CAGCCGCCTC	CGCCACCGGG	GTCTTCCCCG	CCAAGGTGCT	550
	20	GGGGCTCCGC	GTTTGCGGCC	TCTACCGCGA	GTGGCTGAGC	CGCACCGAGG	600
2 0 0 25 0 0		GCGACCTGGG	CCAGCTGCTG	CCCGGGGGCT	CGGCCTGAGC	GCCGCGGGGC	650
	25	AGCTCGCCCC	GCCTCCTCCC	GCTGGGTTCC	GTCTCTCCTT	CCGCTTCTTT	700
and Amil	30	GTCTTTCTCT	GCCGCTGTCG	GTGTCTGTCT	GTCTGCTCTT	AGCTGTCTCC	750
Andreas		ATTGCCTCGG	CCTTCTTTGC	TTTTTGTGGG	GGAGAGGGGA	GGGGACGGGC	800
The state of the s	35	AGGGTCTCTG	TCGCCCAGGC	TGGGGTGCAG	TGGCGCGATC	CCAGCACTGC	850
-	40	AGCCTCAACC	TCCTGGGCTC	AAGCCATCCT	TCCGCCTCAG	CTTCCCCAGC	900
	40	AGCTGGGACT	ACAGGCACGC	GCCACCACAG	CCGGCTAATT	TTTTATTTAA	950
	45	TTTTTTGTAG	AGACGAGGTT	TCGCCATGTT	GCCCAGGCTG	GTCTTGAACT	1000
		CCGGGGCTCA	AGCGATCC 10	018			

(2) INFORMATION FOR SEQ ID NO:7:

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(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1018 bases

- (B) TYPE: nucleic acid (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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CACTTCCCTC GGCCCTAGTC GGTCCCCGGT CGTACTCGGC CTCCCTCCCT 50 10 TCAGACCTTC TGGGGGTCTG ACTAAGGAGT CAGAGTGAAG AAGGGGTGAA 100 CCTCCGGTTC TAGGCAGTCT GTGTGTCGGA ACGCGTGGAG GAGTGGTTTA 150 15 TGCGACTCGT CGACGAGGTC CTTATACACG TCGAGGTCCC TCTGGGGAAG 200 CCCGACGGGT CGAAGAGCGG CGCGCCCGAC GGCCACCGGC CGGACTCGCG 250 20 GGGCCGAGGC TCGGTGCGCC CCGACGGTCA CGTGCTCGCC GACGCCGACC 300 I 25 TGCGCCGCCG CGACCGGCGC GACGGGGGCG ACGACCTGCG TCACACAGCG 350 GCGGTCCGGC TCGACTTGGG CGCGCGCGC GCGGACGACG CGGCGGACCT 400 **3**0 CCTGCGCCGC GCGGTCCGGG CCCGGGACCC GCGGCGCAC CTCCGGAACG 450 ACCGGCGCGA CCCGCGGCGG TTGGCGCCCG GGGCCCGGCT CGGGGGGCGG 500 ₫ 35 CGGTGGCGGA GTCGGCGGAG GCGGTGGCCC CAGAAGGGGC GGTTCCACGA 550 40 CCCCGAGGCG CAAACGCCGG AGATGGCGCT CACCGACTCG GCGTGGCTCC 600 CGCTGGACCC GGTCGACGAC GGGCCCCCGA GCCGGACTCG CGGCGCCCCG 650 45 TCGAGCGGGG CGGAGGAGGG CGACCCAAGG CAGAGAGAAA GGCGAAGAAA 700 50 CAGAAAGAGA CGGCGACAGC CACAGACAGA CAGACGAGAA TCGACAGAGG 750 TAACGGAGCC GGAAGAAACG AAAAACACCC CCTCTCCCCT CCCCTGCCCG 800

	TCCCAGAGAC AGCGGGTCCG ACCCCACGTC ACCGCGCTAG GGTCGTGACG 850)
5	TCGGAGTTGG AGGACCCGAG TTCGGTAGGA AGGCGGAGTC GAAGGGGTCG 900)
	TCGACCCTGA TGTCCGTGCG CGGTGGTGTC GGCCGATTAA AAAATAAATT 950)
10	AAAAAACATC TCTGCTCCAA AGCGGTACAA CGGGTCCGAC CAGAACTTGA 100	0 (
15	GGCCCCGAGT TCGCTAGG 1018	
	(2) INFORMATION FOR SEQ ID NO:8:	
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 201 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
11 11 25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
17 17 25 25	Met Ser Arg Arg Glu Gly Ser Leu Glu Asp Pro Gln Thr Asp Se 1 5 10	er L5
30	Ser Val Ser Leu Leu Pro His Leu Glu Ala Lys Ile Arg Gln Th 20 25 3	ır 30
V Marions A to Propose A to Propose A to Marion A to M	His Ser Leu Ala His Leu Leu Thr Lys Tyr Ala Glu Gln Leu Le 35 40 4	eu £5
35 	Gln Glu Tyr Val Gln Leu Gln Gly Asp Pro Phe Gly Leu Pro Se	er 50
40	Phe Ser Pro Pro Arg Leu Pro Val Ala Gly Leu Ser Ala Pro Al 65 70 7	la 75
40	Pro Ser His Ala Gly Leu Pro Val His Glu Arg Leu Arg Leu As	qe 0e
45	Ala Ala Ala Leu Ala Ala Leu Pro Pro Leu Leu Asp Ala Val Cy 95 100 10	-
	Arg Arg Gln Ala Glu Leu Asn Pro Arg Ala Pro Arg Leu Leu Ar 110 115 12	
50	Arg Leu Glu Asp Ala Ala Arg Gln Ala Arg Ala Leu Gly Ala Al 125 130 13	
	Val Glu Ala Leu Leu Ala Ala Leu Gly Ala Ala Asn Arg Gly Pr 140 145 15	

	Arg	Ala	Glu	Pro	Pro 155	Ala	Ala	Thr	Ala	Ser 160	Ala	Ala	Ser	Ala	Thr 165
5	Gly	Val	Phe	Pro	Ala 170	Lys	Val	Leu	Gly	Leu 175	Arg	Val	Cys	Gly	Leu 180
	Tyr	Arg	Glu	Trp	Leu 185	Ser	Arg	Thr	Glu	Gly 190	Asp	Leu	Gly	Gln	Leu 195
10	Leu	Pro	Gly	Gly	Ser 200										